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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AE002409 Neisseria	AX011576 Sequence		AX011574 Sequence	AX011572 Sequence		U32853 Pseudomonas	U49151 Pseudomonas	AE004511 Pseudomon	U30799 Azotobacter	AE004037 Xylella f	AX011580 Sequence	AF293977 Aeromonas	AE004859 Pseudomon	U31512 Rhizobium m	U07352 Brucella ab	L09274 Brucella ab	AE004142 Vibrio ch	U32495 Escherichia	U15661 Escherichia	AE000402 Escherich
SUMMARIES	;	di .	AE002409	AX011576	NMA322491	AX011574	AX011572	AX011578	PAU32853	PAU49151	AE004511	AVU30799	AE004037	AX011580	AF293977	AE004859	RMU31512	BAU07352	BRUHTRAH	AE004142	ECU32495	ECU15661	AE000402
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Continuation (2 of U29172 Pseudomonas AF163841 Myxococcu AB040030 Shigella AE000125 Escherichia U70214 Escherichia AR095624 Sequence X1248 S.typhimuri A8037634 Sequence AR084295 Sequence AR084	U/03/5 refsills en U/03/51 Brucella ab AR000272 Sequence 1511011 Sequence 7 178681 Sequence 7 L20127 Rochalimaea AE00132 Thermotog AE001355 Chlamydia Y13616 Bradyrhizob	BCT 25-MAY-2000 strain MCS8 section 51 of 206 of	<pre>vision: Neisseriaceae; rg,J., Jeffries,A.C., Hood,D.W., Pedfen,J.F., Hoody,R., Peterson,J.D., White,O., Fleischmann,R.D.,</pre>	Parksey, D. S., Blair, E., Utterback, T.R., Khouri, H., 1ato, V., Masignani, V., .O., Fraser, C.M., Moxon, E.R., a meningitidis serogroup B rg, J., Jeffries, A.C.,, Hood, D. W., Peden, J.F.,, Hood, D. W., Peterson, J. D.,, White, O., Fleistchmann, R. D.,	Utterback, T.R., Khouri, H., Tuterback, T.R., Khouri, H., Tato, V., Masignani, V., To., Fraser, C.M., Moxon, E.R., e for Genomic Research, 9712 50, USA
22 196 14.1 110000 2 ECOUW67_1 24 183.4 13.1 18424 1 AF163841 25 181.2 13.0 1476 1 AB040030 26 178 12.8 10199 1 AB0400125 27 178 12.8 10199 1 AB000125 28 176.4 12.6 1854 81 AR05524 30 176.4 12.6 1855 2 ECHTRA 31 175.6 12.6 1980 81 AR037534 31 175.6 12.6 1980 81 AR037534 31 175.6 12.6 1980 81 AR037534 32 175.6 12.6 1980 81 AR037534 33 175.6 12.6 1980 81 AR037534 34 175.6 12.6 1980 81 AR037534 35 175.7 12.6 1980 81 AR037534 36 175.7 12.6 1980 81 AR037534 37 175.7 12.6 1980 81 AR037534	157.2 157.2 11.3 154.2 11.1 154.2 11.1 154.2 11.1 154.2 11.1 1791 149.6 10.7 11201 148.2 10.6 1781 147.6 10.6 2778	AEO02409/c AEO02409 10531 bp DNA LOCUS DEFINITION Neisseria meningitidis serogroup B s ACCESION AEO02409 AEO02098 VERSION AEO02409 1 GI:7225757	¥	Cittone, H., Clark, E.B., Catcko, A., Parksey, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Qin, H., Vamathevan, J., Gili, J., Scarlatco, V., Masignani, V., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappoli, R. and Venter, J.C. TITLE Complete genome sequence of Neisseria meningitidis serogroup B strain MC58 JOURNAL Science 287 (5459), 1809-1815 (2000) MEDLINE 20175755 PUBMED 10710307 REFERENCE 2 (bases 1 to 10531) AUTHORS Tettelin, Saunders, N.J., Heidelberg, J., Jeffries, A.C., Dodson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Eleischmann, R.D., Dourhorty, B. A. Mason, M.C., Author, A. Eleischmann, R.D., Dourhorty, B. A. Mason, M. C., Salzberg, S.L., White, O., C. Plair, F.D., Alley, M.C., B. L., Walson, M. C., Salzberg, S.L., Walson, W. C., Salzberg, S.L., Walson, W. C., Gwinn, M. C., Salzberg, S.L., Walson, W. C., Salzberg, S.L., Salzberg, S.L., Salzberg, S.L., Salzberg, S.L., Salzberg, S.L	Continue, Trans, Table, Transcriptor, Carlone, M. Carlone, H., Clark, E.B., Cotton, M.D., Utterback, Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Ma Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser Rappuoli, R. and Venter, J.C. TITLE Direct Submission JOURNAL Submitted (17-MAR-2000) The Institute for Genom Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers Source //organism="Neisseria meningitidis MC58 / Strain="MC58"

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gene CDS

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EVGGTSGLVTFEDIISOJVGEIEDBEFDEDDSADNIHAVSSERRIHAATEIEDINTFF
GTEYSSEEADTIGGLVIQELGHLPVRGEKVLIGGLQFTVARADNRLHTLMATRVK"
complement (7301. 7810)
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SPDLRQLGAMPYGGYKLEGEAFKDVVKLISRGGLESMFFYQTIVILGMSLGGLLFAL
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HSRNLSRTLEDAGTVINPLVPWSVCGVFISHALGVPVWEYLPYAFFCYLSLALTLEG
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BOZDALILAAAGLQRKLLDGRIRMLLSESDSJLAAGGGALGTEIAAHREDLYEVLKP
LNHGVTNACVYAERALARALGGSCQYPLAAYCTEENGLLTLRGLYGHPDGSVVLRADA
OAPAEYADALGRAYAKKLADDGARELIGAVLNTEN"
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                                                            Score 1322.2; DB 1;
Pred. No. 1.2e-234;
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KTIIRTLYSNPASHGANTIALVLKNDDLKAQWIAELDEMRGRIKAMRQKFVGLLKAKG
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Neisseria meningitidis serogroup A strain Z2491 complete genome;
segment 3/7.
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Centre are
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/gene="NMA0699"
/note="NMA0699, pseudogene, probable ABC transporter
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Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
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Neisseria meningitidis
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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Details of N. meningitidis sequencing at the Sanger Cent available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/)
Location/Qualifiers
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/organism="Neisseria meningitidis"
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/yeu- name/ // possible ribonuclease BN, len: 408 aa; similar to SW:RBN_ECOLI (EMBL:L19201), rbn, Escherichia coli ribonuclease BN (EC 3.1...), fasta scores; E(): 2.3e-28, 34.3% identity in 268 aa overlap. Longer than rbn at the C-terminus. Also similar to TR:08549 (EMBL:AF067083) Vitreoscilla sp. hypothetical protein (376 aa), fasta scores; E(): 0, 45.0% identity in 333 aa overlap. Contains a region similar to NMA0677, fasta scores; E(): 4.3e-08, 64.4% identity in 45 aa overlap.
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ALVPVLTVWYAVASIFPVFDRWSDSFVSFVNQTIVPQGADMVFDYINRFREQANRLTA
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GEARRRGFDSRGRFDDVLKILLLLDAAQKEGKALPVQEFRRHINMGYDELGELLEKLA
RHGYIYSGRQGWVLKTGADSIELNELFKLFVYRPLPVERDHVNQAVDAVMMPCLQTLN
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868. .912
/gene="NMA0699"
                 to C-termini of many ABC
protein, len: 336 bp; similar to C-termini of many ABu transporters e.g. TR:046973 (EMBL:047048), mtfB, Escherichia coli microcin transport protein (707 aa), fasta scores; E(): 2.6e-19, 53.2% identity in 111 aa overlap. Contains PS00211 ABC transporters family signature. NMA0686 may be the remainder of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMA0701 (pseudogene)"
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/note="Core DNA uptake sequence: gccgtctgaa"
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1376. 1385
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complement(1101. .2327)
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                                                                                     //note-"NWA0702, len: 219 aa; similar to TR:052925
(EMBL:250189), exsB, Rhizobium meliloti putative regulator
of succinoglycan biosynthesis (not a transcriptional
regulator) (234 aa), fasta scores; E(): 3.18-15, 32.7%
identity in 205 aa overlap. Also similar to many
hbacterial prothetical proteins e.g. Sw:RAAX.HABIN
(EMBL:032798), HII191, Hemophilus influenzae hypothetical
protein (196 aa), fasta scores; E(): 0, 79.2% identity in
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DabkiHidGWQVVEWADGYPLEAVCDDYREAVCDDYREAVPALKAAWFG
DABKIHIDGWQVVEWADGYDIAVSETPRTKMSENAPRLYFAWVGGYRAGGLAEAHAF
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PARIGEGGGYLPI"
3782. 3791
/gene="NMA0703"
                                                                                                                                                                                                                                                                                      /product-"hypochetical protein NMA0702"
/product-"hypochetical protein NMA0702"
/productein_d="CAB83989.1"
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/translation-"MSNOKALVIFSGGODSTTCLIQAIOTYGRENVOAITFOYGORHA
VELERRAMIAGOLGVKOTVULDSLAMROTHNALMDDTAALTARENCVANTEVUGENAL
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MYLTKAQTWAALAADEMGALDYIREQTHTCYNGIVGGCRECPSCILRERGLAEYLESKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notew-NMA0704, len: 140 aa: similar to many hypothetical proteins e.g. SW:YB90_HAEIN (EMBL:U32798), H11190, Haemophilus influencae hypothetical protein (141 aa), Hasta scores; E(): 5.1e-32, 58.0% identity in 138 aa overlap. Shows very weak similarity to eukaryotic e.pruvoy1-tetrahydropterin synthases e.g. SW:PTPS_RAT (EMBL:W77850), pts, Rettus norvegicus 6-pyruvoy1 tetrahydrobiopterin synthase.
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/gene-"NMA0704"
/note-"Pfam match to entry PF01242 PTPS, 6-pyruvoy1
tetrahydropterin synthase, score 10.80, E-value 1.7e-06"
/gene-"NMA0704"
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/note~"Core DNA uptake sequence: gccgtctgaa"
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/protein_id-"CAB83990.1"
/db_xref-"GI:7379428"
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/product="hypothetical protein NMA0704"
/protein_id="CAB83991.1"
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.5e-234;
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Pred. No. 8.5e-
0; Mismatches
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/transl_table=11
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/transl_table=11
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3558. .4076
/geneu"NMA0703"
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/gene≃"NMA0704"
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2871, .3530
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/gene-"NMA0702"
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llarity 96.9%;
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1081 cccgtcatggtcggcgcattacgccgggaaagagtcagcctcggcgtatggcgcaaa 1140 	1141 ggcgaagaaatcacaatcaaagccaagctgggcaacgccgcggggatacatac	1201 tccaaaacagatgaagcccctacaccgaacagcaatccggtacgttctcggtcgaatcc 1260 	1261 gcaggcattacccttcagacacataccgacagcagcgaaacacctcgtcgtcgtacgg 1320 	1321 gtttccgacgcggcagaacgcgcaggcttaaggcacggcgacgaaatcctagccgtcagg 1380 	1381 gcaagtccccgtcaa 1395 	אויט אייט אויט אייט אייט 10.	10 25 - 10	UNCES Neisseria meningitidis. ORGANISM Neisseria meningitidis Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;	EFERENCE (bases 1 to 1500) AUTHORS Ruelle, J.L. TITLE Basboll and and proteins from neisseria meningitidis	RUELLE JEAN LOUIS (BES); SMITHKLINE BEECHA Location/Qualifiers	Clais	1500;	*ative v, mismatches /J, accaatacttcgctttggcggcactgtgtgccafactattggcgcactgtflllllllllllllllllllllllllllllllllll	tgcgaaaaggcaggcagctttttcggtgcggacaaaaagaagcatccttcgtagaacgc flll	atcgaacaccaaagacgacggcagtgtcagtatgctgctgccgactttgcccaactg	gttcaaagcgaagcccggcagtcgtcaatattcaggcagccccgccccgcccaacaa 24	ctac 3	241 AACGCCGCTTCTCCGAACCGATTCCGACCGACGCGACGC

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Location/Qualifiers
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Sequence 7 from Patent
AX011578
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                                                                                                        Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                             90.2%; Score 1258.2; DB 2; Length 1500; llarity 94.3%; Pred. No. 1.1e-222; Conservative 0; Mismatches 78; Indels 1;
                                                                                                                                                       BIOLOG (BE)
                                                                                                                                       meningitidis
                                                                                                                         l (Usestale, J.L.)
Ruelle, J.L.
BasbOld dna and proteins from neisseria mt...
Patent: WO 995872-A 04-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM
Location/Qualifiers
                                                 BCT
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                                             AX011572 1500 bp DNA
Sequence 1 from Patent W09955872.
AX011572
                                                                                                                                                                            /organism="Neisseria
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468 c 393 g
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meningitidis
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                                                                                                               Neisseria.
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GCAAGTCCCCGTCAA 1394
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Best Local Simi
Matches 1316;
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Ruelle, J. L.
Basbolls dna and proteins from neisseria meningitidis
Patent: WO 9955872-A 04-NOV-1999;

RUELLE JEAN LOUIS (BE): SMITHKLINE BEECHAM BIOLOG (BE)
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Neisseria meningitidis
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Neisseria.
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/codon_start=1
/transl_table=11
/product="Mucc"
/product="d1:1184683"
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STROKLEDFRAMARGOLSIPDLEGLPPWERDFLERSIPQVPRNRRGQREAGSLGSGFT
ISNDGYILTNNHVVADADEILVRLSDRSEHFAKLIGAPRSDYDVLKIEAKNIGHEPTLKL
GDSNKLKVGEWVLATGSPFGFDHSVTAGIVSAKGRSLPNESYVPFIQTDVAINPGNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boucher, Microbiology, University 7703 Floyd Curl Dr., San Antonio,
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1961)
Boucher, J.C., Martinez-Salazar, J., Schurr, M.J., Mudd, M.H., Yu, H.
and Deretic, V.
Two distinct loci affecting conversion to mucoidy in Pseudomonas
aeruginosa in cystic fibrosis encode homologs of the serine
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complete cds.
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                              TGGGCGTGATTATTCAAGAAGTATCCTACGGTTTGGCACAATCGTTCGGTTTGGACAAAG
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision;
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/db_xref="GI:1184684"
                                                                                                                                                                Direct Submission
Submitted (31-UUL-1995) John C.
of Texas Health Science Center,
TX 78240, USA
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Pseudomonas aeruginosa mucC
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/organism-"Neisseria m
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Matches 1079; Conservative
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QEVKRÜLAESGELÜKPSGALVÄQLVEDGPAAKGGLQVGDVILSLNGGSINESADLPHL
VGNWK PGDKINLDVIRNGQRKSLSMAVGSLPDDDEEIASMGAPGAERSSNRLGVTVAD
LITAEORKSLDIQGGVVIKEVODGOFAAVIGLRFGDVITHLDNKAVTSTKVFADVAKALP
KNRSVSMRVLRQGRASFITFKLAE"
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PAU49151 4587 bp DNA BCT 13-MAR-1996
Pseudomonas aeruginosa alternate sigma factor (algU), mucA, mucB, mucC and mucD genes, complete cds.
U49151 U24569 U08380 L04794 L02119
U49151.1 GI:1220191

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RESULT PAU49151

LOCUS

ACCESSION

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Churr, M.J., Yu, H., Boucher, J.C., Hibler, N.S. and Deretic, V. Multiple promoters and induction by heat shock of the gene encoding the alternative sigma factor Algu (sigma E) which controls mucoidy in cystic fibrosis isolates of Pseudomonas acruginosa J. Bacteriol. 177 (19), 5670-5679 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A (bases 252 to 488)
Martin, D.W., Schurr, M.J., Yu, H. and Deretic, V.
Analysis of promoters controlled by the putative sigma factor Algu
regulating conversion to mucoidy in Pseudomonas aeruqinosa:
relationship to sigma E and stress response
J. Bacteriol. 176 (21), 6688-6696 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 (sites) Yu,H., Schurr,M.J. and Deretic,V. \\ Functional equivalence of Escherichia coli sigma E and Pseudomonas aeruginosa Algu: E. coli rpoE restores mucoldy and reduces sensitivity to reactive oxygen intermediates in algU mutants of P.
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Boucher,J.C., Martin,D.W., Schurr,M.J., Deretic,V., Yu,H., Mudd,M
and Martinez-Salizar,J.
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7. (Dassa 1 to 4587)
Boucher, J.C., Martinez-Salazar, J., Schurr, M.J., Mudd, M.H., Yu, H.
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                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Proc. Natl. Acad. Sci. U.S.A. 90 (18), 8377-8381 (1993)
93391358
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MarLin,D.W., Schurr,M.J., Mudd,M.H. and Deretic,V.
Differentiation of Pseudomonas aeruginosa into the
Differentiation of Pseudomonas aeruginosa into the
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Martin, D. W., Holloway, B. W. and Deretic, V.
Characterization of a locus determining the
Pseudomonas aeruginosa: Algu shows sequence
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/traislation="MITLKRCMAAMVALLALSLAMTARAELDDFTPLVEQASPAVVNI
STROKLPDRAMARGQLSIPDLEGLPPWFRDFLERSIPOVPRNPRGQOREAGSLGSGFI
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GDSWIKLKVGEWVLAIDSPFCFINNSCHFKYNG IVSAKGRSLPNESVVPFIOTDVAINBGNSG
GPLLNLGGEVVGINSQIFTRSGGFMGLSFAIPTDVALNVADOLKKAGKVSRGWLGVVI
OBVNKDLAESFCLDKPSGALVAAQLVEDGPAARGGLQVGDVILSLNGQSINESADLPHL
VGNMKFQGRKILDVIRNGQRKSLSMAVGSLPDDEEIASMGAPGAERSSNRLGVYAD
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/db_xref="GI:1220193"
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1087. 1671
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          end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="conversion to mucoidy; required for algD transcription"
                                                                                                                                                                                                                                                                                                                                                                                  promoter P2; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P1; 3'
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                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                          /note="AlgU-dependent transcription start site for promoter P3; 3' end is unknown"
                                                                                                                                                                                                                                                                                                            site
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                                                                                                                                                                                                                                                                                                            start
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                                                                                                                                                                                                                                                                                                            /note="AlgU-dependent transcription
promoter P3; 3' end is unknown"
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/note="P3 promoter"
226. .230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389. .421
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                                                                                                                                                                                                                                                                                                                                                                                                                                    389. .394
/note="P1 promoter"
389. .421
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/note="Pl promoter"
                                                                                                                                                                                     'note="P3 promoter"
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474. 1055
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1680.
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1087.
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/gene="mucA"
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GNSGDGIAMAWRAGCRVGNLEFNQFHPTCLYHPQAKSFLITEALRGEGALLRLPNGER
FWPRFDPRGELAPRDIVARAIDHEMKRLGIDCVYLDISHKPAEFIKAHFPTVYERCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGIDITQQPIPVVPAAHYTGGGVLVDOHGHTDVPGLYAIGETTFTGLHGANRMASNSL
LECEYVARSAAADMLQRLGPTPVPESLESWDASQVTDSDEDVIIAHNDELRRFRWDY
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1982. . 4553
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VYERNGSFSTHEIWHRYESDGAVRERLQLDGARQEVVRVDGRTGCI SGGLADQLADA
OLWPVRKFDPSQLASWYDLRVGGSRAVGRPRAVLAVTPRDGIRYGFELLIDRGTGLP
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TRDEQHNHEEGSFEYHLTREGGHSHRRIIHAADATGAAIFNTLLAQARRRPNIELLSQ
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                                                                                                             /product~"conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRLPIYLRQHVQQSAVSGTESALPYARAASLENR"
5188. .6138
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                                                      /codon_start-1
/transl_table-11
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4595. .5179
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5188. .6138
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Stover,C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M.,
Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y.,
Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stover, C.K., Pham, X.-O.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Stover, C.K., Pham, X.-O.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, P.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Direct Submission
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LRIGLRDASFALRALGIDTPAESGRIARHGDLLAVALGDGRVELWVPAQRAEAVLATL
REHSREAPLDDWLLGQVRAGIGQVFGATRELFIPQMINLQAVGGVSFKKGCYTGGEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MADPAFHTPLVHEGILAVRGPDAAKFLQGQLTCNLAYLNDETSS
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LQDDAVADGRISLGSAEGAPLVLLNLPYTLDSDREIQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Mashington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA Location/Qualifiers
                                              3948 TCCAGGAAGTGAACAAGGATCTCGCCGAGTCCTTCGGCCTCGACAAGCCGTCCGGCGCGC 4007
                                                                                                        tcgtcctcagcctcgacggcggagaaatacgttcttccggcgaccttcccgtcatggtcg 1093
                                                                                                                                                                                                                                                                     4127
ttcaggaagtatcctacggttttggcacagtcgttcggtctggataaagccagcggcgat 973
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529 of the complete
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                         gegecattacgeegggaaaaagaagteageeteggegtatggegeaaaggega 1145
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Nature 406 (6799), 959-964 (2000)
20437337
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/transl_table=11
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AE004511.1 GI:9946646
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                  Query Match
                               Best Local
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GHYFMMGDNRDNSNDSRYWNDPKIPKDLLGMVPDRNIVGKAFAVWMSWPDPKMSNLPN
                                                                                                              biosynthesis
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VSKRLQTDDGGQMVTVVGEVPLGTAERVALSIRPEAAAQK"
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                                                                                                                                                                                                                                                                                                        precursor"
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AVU30799 2027 bp DNA BCT 31-MAY-1996
Azotobacter vinelandii MucC (mucC) and MucD (mucD) genes, complete
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Azotobacter vinelandii
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGGCGCGGACCGCGCAGCGAGCGTGCTGAAGATCGAGG---CGAAGAACCTGC
                                                                                                                                                                                                                                                                                                         toggttcgggcttcatcatcagcaaaacggctacatcctgaccaatacccacgtcgttg
                                                                                          ccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactca
                                                                                                                                                                           CCGATGCCGACGAGATCCTGGTGCGCCTGTCCGACCGTAGCGAGCACAAGGCCAAGTTGA
                                                                                                                                                                                                                                                                                                                                                            gcgcgcccttcggctttgacaacagcgtgaccgccatcgtgtccgccaaaggcagaa
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Martinez-Salazar,J.M., Moreno,S., Najera,R., Boucher,J.C.
Espin,G., Soberon-Chavez,G. and Deretic,V.
   Length 10977;
                                     3;
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                  5e-58;
                                   0; Mismatches
Score 365.6;
Pred. No. 3.5
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us-09-388-090-3.rge

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GenBank Accession Number U07352"
                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded
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Characterization of the genes coding for the putative sigma factor AlgU and its regulators MucA, MucB, MucC, and MucD in Azotobacter vinelandii and evaluation of their roles in alginate biosynthesis 96178940
                                                                                                  2 (bases 1 to 2027)
Martinez-Salazar, J.M., Moreno, S., Najera, R., Boucher, C., Espin, G. Soberon-Chavez, G. and Deretic, V.
Direct Submission
Submitted (30-JUN-1995) Jaime M. Martinez-Salazar, Microbiology, UTHSCSA, 7703 Floyd Curl Drive, San Antonio, TX 78284, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttctacgaatttttcaaacgcctcgtcccgaacatgcccgaaatcccccaagaagca 354
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                                                                                                                                                                                                                                                                               /organism-"Azotobacter vinelandii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 274.8; DB 2;
Pred. No. 2.9e-41;
0; Mismatches 362;
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                                                                                                                                                                                                                                       Location/Qualifiers
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Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Simpson, A.J.G., Reinach, F.C., Arruda, P., Balad, G.S., Haptista, C.S., Alves, L.M.C., Araya, J.B., Balad, G.S., Haptista, C.S., Barcos, M.H., Bonacorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costu, F.F., Costu, M.C.R., Costu-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Facincani, A.P., Ferreira, A.J.S.,
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1 (bases 1 to 1215)

2 (bases 1 to 1215)

2 (bases 1 to 1215)

3 (bases 1 to 1215)

4 (bases 1 to 1215)

5 (bases 1 to 1216)

Terenzi, M.L., Siqueira, W.J., de Souza, A.A., de Souza, A.P.,

Terenzi, M.F., Truffi, D., Tsai, S.M., Tsuhako, M.H., Vallada, H., Van Sluys, M.A., Varjovski-Almeida, S., Vettore, A.L., Zago, M.A., Zatz, M. Meidanis, J. and Setubai, J.C.

The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil

Nature 406 (6792), 151-157 (2000)
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933 CAAGGGTTCGAAT---CTCCCCACAGTCAAACTGGGACGTACCGACCAATTGACAGTCGG
                                                                                                                                                                                            594 cgaatgggtcgctgccatcggcgcccltcggctltgacaacagcgtgaccgccggcat
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AE004037.1 G1:9107394
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                 Frohme, M. Ferlob. A., Fradga, J.S., Franco, M.C., Ferletter, V.C., Ferletter, V.C., Ferletter, M. Caruber, A., Gardinan, G. H., Goldman, M. H.S., Gomes, S. L., Gruber, A., Ho, P. L., Hoheisel, J.D., Junqueira, M. L., Kemper, E. L., Kitfailma, J. P., Krieger, J.E., Kuramae, E.E., Largret, F., Lambais, M. R., Leite, L.C.C., Lemos, E.G. M., Lemos, M. V.F., Lopes, S. A., Lopes, C.R., Machado, M.A., Machara, A. M. B. N., Martins, E.A. L., Martins, E.M. F., Mariakua, A.Y., Marques, M.V., Marcaca, E.C., Miyaki, C.Y., Monteiro, Vitorello, C.B., Moon, D. H., Nagai, M.A., Nascimento, A. L. T.O., Netto, L.E.S., Nhani, Jr., A., Nobrega, F.G., Nunes, L.R., Oliveira, M. P., Geoliveira, M. C., de Oliveira, R.P., Pereira, P. Pesquero, J.B., Quaggio, R.B., Pereira, G. A., Paris, A., Pesquero, J.B., Quaggio, R.B., Roberto, P.G., Rodrigues, V., de M. Rosa, A.D., de Rosa Jr., V.E., de Say, R.G., Santelli, R.V., Sawasaki, H.E., da Silva, A.C., Silvestri, M.L.Z., Siqueira, W.J., de Souza, A.P., Tereizi, M.F., Truffil, D., Tsai, S. M., Tsukako, M.H., Vallada, H., Van Sluys, M.A., Verjovski-Almeida, S., Vettore, A.L., Zago, M.A., Zatz, M., Meidanis, J. and Setubal, J.C.
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TPAPQLVAGLPDFTQLVDQVGPGVVNIETVITRKKVGKRRGIPLDNDIPEFFRRFFGP
DFQMPNQPRGGQDDEGGLAGRGMGSGFIISKDGYILTNHHVITGASEVTIKLTDRREF
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SALGRSTSDDQRYVPFIQTDVPINQGNSGGPLLNTRGEVIGINSQIFSASGGYMGISF
AIPINLAINAAEQIRKTGKVQRSMLGVEIGPIDALKAQGLGLPDSRGALVNNIPPHSP
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LNQDATASEDEDDTAPSKPETSANVELLGLQVENLSAAERREKLASSQNAKGGVRITAV
TAPWARNANPPLVEGLVILRIGRTPVSNVAELNRVLGNYKKGDVIMLLVTNGRGTFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GI|1184684 (percent identity: 47 %/query alignment coverage: 91.2 %/subject alignment coverage: 98.9 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder/start codon shift: -48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to SP|P07682 (percent identity: 69 %/query alignment coverage: 99.5 %/subject alignment coverage: 100.0 %); identified by sequence similarity; putative; ORF located using climmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing and 5, Campinas, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-2000) organization for Nucleotide Sequencing analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas,
Ferreira, V.C.A., Ferro, J.A., Fraga, J.S., Franca, S.C.,
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/protein_id="AAF85040.1"
/db_xref="GI:9107395"
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/protein_id="AAF85041.1"
/db_xref="GI:9107396"
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/organism="Xylella fastidiosa"
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/transl_table=11
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/gene="XF2243"
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/gene="XF2242"
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13083-970, Brazil
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/product="Garp binding protein"
/product="Tap Binding protein"
/product="TapR85642.1"
/db_xref="Garp binding protein"
/db_xref="Garp binding protein p
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LIFESGDPHTKHPRVSCTLGELKLRTEGEGSSRRLAEQDAASHAIDQLDSNK"
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/db_xref="G1:9107394.1"
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VYQKYYSLOTAMKSLKKELGANSDLPPSTIEEFFKRINDSFDNVKKENIKFEKIRDG
WKMKINFEILRKRIGNMDLVGTFDTEQDLTSRDIK"
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TKIIPIGKPNRGDVAVFKPPHKPDENWIKRVIGLPGDRIGFHGDTLYINGEPVKYILK
GQYIGKNAGVPDFTLLIEELPNHPHTILESIGRGREEGEGEWVVPPGQYFVWGDNRDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP|P00803 (percent identity: 40 %/query alignment coverage: 113.5 %/subject alignment coverage: 93.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to SP|P43728 (percent identity: 51 %/query alignment coverage: 97.3 %/subject alignment coverage: 96.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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/protein_id="AAF85043.1"
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/transl_table=11
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/trans1_table=11
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/gene="XF2247"
5594. .6490
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/gene="XF2244"
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/gene="XF2244"
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/gene="XF2247"
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GTAAAAACAGGCAAAGGCAACGCAGTATGCTCGTGTGGAAATCGGCCCTATCGCCAC 1010
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                                                                                                                                                                                                                                                                                                                CCCACAGCCCGGCCGAAAGCAGGGATTGAAGTCGGTGACGTCATCCGCTCAGTGAACG 1130
                                                                                                                                                                                                                                                                                                                                                                                    1131 GCAAAGTAATCAGTAGCTTCAGCGATCTGCCTCCACTGATCGGCATGATGCCGCCAGGCA 1190
                                                                                                                                                                                                                                                                                                                                                          geggagaaataegttetteeggegaeetteeegteatggteggegeeattaegeeeggaa 1111
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Basboll 3 dna and proteins from neisseria meningitidis
Patent: WO 9955872-A 04-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM BIOLOG (BE)
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Sequence 9 from Patent W09955872.
AX011580 GI:9998109
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/db_xref~"taxon:487"
120 c 102 q
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RHRLLGIATFPEGQIVLVDTPGLHREQKHPMNRLMNRTARGSLEDVDAALLYTESTHW
NEEDTLAXNLLNDTGIPVYLVINKIDRFKDKSALLPFLTHINBNHFFTTIHPVSALKR
KGLETLVSDLLALLPEGDPMFSEDEITDRSQRFLASELVREQVMRQLGEELPYATTVE
IEYFTBNTGLFRIGALLWVBRESQRALVIGKGGARLKEIGVKARQQMERLFQTKVFLE
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                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MLIEHEVAFVLHVRPWRETSLLVEVLTOAVGRLGLIARGYOGLK
KOTLRAALOPLOWIRFSAIORGELGOLROABALDTAPRLKGEAMLASFYINELLLRLV
PRHAPVNELYLAYSOTRERLRTSDSLAWSLRLFEREILETLGYGFNLECDANGTPLDP
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                                                                                                                                                                                                                                                          /note="similar to SP|P15027 (percent identity: 35 %/query alignment coverage: 97.1 %/subject alignment coverage: 97.5 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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/protein_id="AAR85047.1"
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larity 56.3%; Pred. No. 8.9e-39;
Conservative 0; Mismatches 431
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/transl_table=11
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/protein_id="AAF85046.1"
/db_xref="GI:9107401"
                                                                                                                                                                                              Jene="XF2248"
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/gene="XF2248"
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Stover.C.K., Pham.X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadnan,S., Yuan,Y., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Pulsen,I.T. complete genome sequence of Pseudomonas aeruginosa PA01, an Opportunistic pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Mestbrook, Radman, S., Yian, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.M., Lory, S. and Olson, M.V.

Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington, Center, University of Washington,
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                                                             cccaacgaaagctacacaccttcatccaaaccgacgttgccatcaatccgggcaattcc
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/transl_table=11
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ELRYGDYALAIGNPFGLGGTVYSGTVSALGRSGLNIENLENFIQTDAAINSGNSGGAL
LNLRGELIGINTALLGPNGGNTGIGFAIPSNNYRDLESQIYKXGERRRGQLTIGTEL
TSBVAKTFGYNKNGAFVNYMPDSAAARAGIKPGDIIVSIDGKAIRSFGELRAKIAT
MGADKQVALGIIRDGKEQTVKVTLKRADDSEILASALHPALEGAKLSTTSEPVSGVAV
SEIDPRSPAAASGLQKGDVIIGVNRLRINSLEELSKALKNKPDVLALNIQRGDSSLYL
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Lin.T.-N., Lin,T.-J. and Liou,C.-M.
Direct Submission
Submitted (No-NG-2000) Agricultural Chemistry, National Taiwan
University, No.1 Roosevelt Road Section 4, Taipei 106, Taiwan
Location/Qualifiers
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                                                                                                                   AF293977 1362 bp DNA BCT 30-AUG-2000
Aeromonas hydrophila htrA-like serine protease (prtS1) gene,
                                                                                                                                                                                                                                                                             subdivision; Aeromonadaceae;
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Pred. No. 6.4e-36;
0; Mismatches 330; Indels
241 AGGCGCGGCGACGAATTCTTGCCGTC-GGGCAAGTCCCCGTCAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1362
/organism="Aeromonas hydrophila"
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                                                                                                                                                                                                                                                                                                                                                           prtS1
                                                                                                                                                                                                                                                                                                                                   Lin, T.-N., Lin, T.-J. and Liou, C.-M. Aeromonas hydrophila strain CKH-29
                                                                                                                                                                                                                                                                                 gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394
                                                                                                                                                                                                                                                         hydrophila
Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="prtS1"
1. .1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="prtS1"
                                                                                                                                                                                             AF293977.1 GI:9945003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.6%;
58.3%;
                                                                                                                                                                                                                                        Aeromonas hydrophila.
                                                                                                                                                                                                                                                                                                                    (bases 1 to 1362)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.6
Best Local Similarity 58.3
Matches 470; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1362
                                                                                                                                                        complete cds.
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                                                                                                                                                                                                                                                           Aeromonas |
Bacteria; |
                                                                                                                                                                                                                                                                                                    Aeromonas.
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                                                                                                                                     DEFINITION
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ORIGIN
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TITLE
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AUTHORS
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                                                                                            AF293977
LOCUS
                                                                                                                                                                            ACCESSION
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SOURCE
                                                                                                                                                                                                                                                                                                                    REFERENCE
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/terrilation="MLTIALSKGRILDDTLPLLAAAGIVPSENPDKSRKLIIPTSLSD VRLLIYRATDDVPTYVEHGAADLGVAGKDVLMEYGGGGLYEPLDLRIANCKLMTAGAIG APEPKGRLRVATKFVNVAKRYYAEGGROVDVIKLYGSMELAPLVGLABKIIDVVDTGN COMPLEMENLEGGELYGISSRLVVNKASMKMQHGRIGSLIDTLRDAVEARRR" complement (6539. . 7804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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FORRSSIINCSAEGASVLGRTASVLARGESLTAHARSAEYRILDEKEA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGVKRLGGARYDVLPDRIETGTYLVAAAATGGRVKLKDTDPT1LEAVLÓKLEEAGAHI
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DRIYHIDRGYEGIEEKLQLLGAKIRRVPG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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complement(5886. .6521)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(6539. .7804)
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                                                                                                                        /transl_table=11
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PLLVDAGQPIRRIAWGTGGAQGXIDQAIAAGVDAYLTGEVSEQTVHSARENGISFIAA
GHHATERYGVQALGDYLGKRFAIEHLFIDCPNPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAMGYGQFMPSSFTKYAVDFDGDGHIDLWNPRDAIGSVANYFKQHGWVSGDRVAVPAS
GRAPSLEDGFKTLYPLDVLASAGLRPQGPLGGHRQASLLRLDMGRNYQYWYGLPNFYV
ITRYNHSTHYAMAVWELGKEVDRVRHRSVVRQD"
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DAAINPGNSGGALVDAAGNLIGINTAIFSKSGGSQGIGFAIPTKLALEVMQSIIEHGQ
VIRGWLGVEVKALTPELAESLGLGEFTAGIVVAGVYRDGPAARGGLLPGDVILTIDKQE
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SASLQALGFEVLPSAANFVFARHPRHDAGQIASTLREQGVIVRHFKQARIDGFLRITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'translation≈"MRRTALALPLFLLVSACSSEPTPPPKPAAKPQARTVISPRPVRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVQPILPLRGDYANNPAAQHFIDRMVSQHGFNRQQLHDLFAQTQRLDWVIRLMDRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYTPPSGPNGAWLRYRKKFVTPGNVQNGVLFWDQYETDLQRASRVYGVPPEIIVGIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VETRWGRVMGKTRIIDALSTLSFSYPRRAEFFSGELEQFLLQARKEGTDPLALRGSYA
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ESSLGSAVIMSAEGYLLINNHVTAGADQIIVALRDGRETIAQLVGSDPETDLAVLKID
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98195, USA
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5, Seattle, WA 98199
Location/Qualifiers
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Box 352145,
                                                                                                                                                                               gene
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                           FEATURES
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VDPDSDAGDRGLKEGRRIYVSNNUQEVNRQTTFSR"

8 a 626 c 626 g 344 t
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Glazebrook, J., Ichige, A. and Walker, G.C.
Genetic analysis of Rhizobium meliloti bacA-phoA fusion results in identification of degP: two loci required for symbiosis are closely linked to degP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (12-JUL-1995) Jane Glazebrook, Department of Molecular
Biology, Massachusetts General Hospital, Wellman 10, MGH, Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sinorhizobium meliloti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
376 ggttcgggcttcatcatcagcaaaacggctacatcctgaccaatacccacgtcgttgcc 435
                                                                                                                                   gaagaaatcacaatcaaagccaagctgggc--aacgccgccgagcataccggcgcatcat 1201
                                                                                                                                                                                                                                                                                                         Activation 2 1974 bp DNA BCT 05-MAR-1996
Rhizobium meliloti RmDEGP (degP) gene, complete cds.
U31512
U31512.1 GI:951169
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Glazebrook, J.
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YFDNIAGVTVRGKVTLAGVTICKVTAVDLDRDSYTGRVTMEINQNVNNLPVDSTASIL
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Search completed: March 22, 2001, 04:06:30 Job time: 4575 sec

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NGSP; polypeptide; peptide; vaccine; immune response; antibody; cellular matrix; adherence domain; ligand; detection; diagnosis; screening; probe; primer; prophylaxis; therapy; ss.
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gonorrhoeae to the host's cellular matrix reducing attachment and/or subsequent invasion. The NGSP polypeptide and its peptide fragments can be used to immunise an animal and produce an immune response. They can also be used as liganda to detect antibodies elicited in response to Neisseria infections and also as antigens or immunogens for inducing Neisseria-specific antibodies which are useful in immunoassays to detect Neisseria in biological specimens. Nucleotides encoding NGSP or its fragments can be used as probes to identify Neisseria in biological specimens by hybridization or polymerase chain reaction amplification. The NGSP polypeptide can also be used in screening assays to identify agents and compounds which useful as diagnostic, prophylactic or therapeutic agents against Neisseria
                                                                                                                                                          The NGSP polypeptide of N. gonorrhoeae has conserved Arg-Gly-Asp and Arg-Gly-Asn motifs near the C-terminus which function as adherence domains for extracellular matrix proteins. Using the NGSP polypeptide as a vaccine produces antibodies which inhibit binding of N.
                        from
Neisseria
                      Ppolypeptide and polynucleotide sequence for diagnosis, prevention or treatment of
                                                                                                                  60-61; 68pp; English
                      NGSP
                      Non-cytosolic NGS
Neisseria useful
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Sequence 1395 BP; 359 A; 438 C; 353 G; 245 T; 0 other;

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                                                                                                              cytotoxic;
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The present sequence is a DNA encoding Neisseria meningitidis NMASP protein. NNASP is a non-cytosolic protein, with antibacterial and antiinflammatory activity. It shows sequence similarity to E. coli DegP (HtrA) protein. NMASP proteins can be used as ligands to detect antibodies elicited in response to N. meningitidis infections. Cytotoxic may be used for diagnosis, therapy or prophylaxis of Neisserial infections such as, bacterial meningitidis and septicaemia.
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Best Local Similarity 99.9
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The present sequence encodes a BASB013 polypeptide isolated from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be employed as research reagents and material for the discovery of treatments and diagnostics for diseases, particularly human discascs. They can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polypucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and das components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists which are bacteristatic) are used for the treatment and antagonists such as upper respiratory tract infection. Invasive bacterial diseases such as bacterial drugs. They are also used in the prevention of adhesion of bacterial drugs. They are also used in the prevention of adhesion of bacterial to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of in-discipled and protession of the physical and propression of the physical and propression of the physical and propression of the physical and proteins and to the physical and progression of the physical and protession of the physical and propression of the physical and protession of the physical and protession of the physical and propression of the physical and protession of the physical and physical a
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                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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99WO-EP02765
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Best Local Similarity
Matches 1355; Conserv
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20-APR-1999;
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us-09-388-090-3.rng

Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.

Neisseria meringitidis

WO9957280-A2

Neisseria meningitidis ORF 986 partial DNA sequence SEQ ID NO:2969

(first entry)

21-MAR-2000

254511;

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novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 24537 to 254576 and 254616 to 255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of immunogenic compositions. The polypeptides and compositions of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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Scalato E, S
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Rappuoli F
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Best Local Similarity 96.9
Matches 1352; Conservative
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Venter JC;
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Tettelin H,
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253015 to 254536, 254577 to 254615, and Y74253 to Y75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 254577 to 254576 and 254616 to 255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
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Ratti (
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Tettelin H, Venter JC;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a BASB013 polypeptide isolated from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may employed as research reagents and material for the discovery of treatments and diagnostics for diseases, particularly human diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence
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t bacterial infections -
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creates and the control of disease, staging of disease, or determining response of an infectious organism to drugs. The determining response of an infectious organism to drugs. The plynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, sercitype, organism or strain identification, identification of mutation in BASB013 sequences, and accomponents of arrays which are used to produce antibodies. The polypeptides can also be used to produce antibodies. The polypeptides and strain discounties and antegonists and antegonists and antegonists. The polypeptides, antibodies, agonists and antegonists and associated as upper respiratory tract infection, antagonists (which are bacteristatic) are used for the treatment and prevention of diseases such as bacteraemia and meningitis, and for the development and screening of antibocterial drugs. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins of thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of xxx sequence 1500 BP: 370 A; 469 C; 392 G; 269 T; 0 other;
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ä 240 360 540 540 180 300 300 420 420 480 480 600 600 999 gccaaaggcagaagcctgcccaacgaaagctacacccttcatccaaaccgacgttgcc 720 9 9 Gaps aacggcagcggcaatgccgaaaccgattccgaccgcttgccgacagcgaccgttctac aacggcagcggcaatgccgaaaccgattccgacccgcttgccgacagcgacccgttctac ggoggattgaacttcggttcgggcttcatcatcagcaaaaacggctacatcctgaccaat ggcggattgaacttcggttcgggcttcatcatcagcaaagacggctatttctgaccaat acccacgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatat acgcacgtcgttaccggcatgggcagtatcaaagtcctgctcaacgacaagcgcgaatat gtcgccgccatcggcgcccttcggcttcgacaacagcgtgaccgccggcatcgtgtcc gccaaaggcagaagcctgcccaacgaaagctacacaccttcatccaaaccgacgttgcc atcgaacaccacaaagacgacggcagtgtcagtatgctgctgcccgactttgcccaactg gttcaaagcgaaggcccggcagtcgtcaatattcaggcagccccggccccaa acggaagagctacccgtcgtcaaaatcggcaatcccaaaaatttgaaaaccgggcgaatgg gtcgctgccatcggcgcgcccttcggctttgacaacagcgtgaccgccggcatcgtgtcc 1, Length 1500; Indels Sequence 1500 BP; 370 A; 469 C; 392 G; 269 T; 0 other; 75; 21; DB Score 1263; D Pred. No. 0; 0; Mismatches 90.5%; 94.6%; Conservative Query Match Best Local Similarity Matches 1319; Conserv 61 61 121 121 181 181 241 241 301 361 421 481 481 541 541 601 661 301 361 421 601 661 Q ۵ م Q g δ q q à g g g 8 ò g ò ò à à à ò ò

Neisseria meningitidis; BASBO13; diagnosis; infection; vaccine; antibiotic; upper respiratory tract infection; bacteraemia; meningitis; invasive bacterial disease; antibacterial; ss. 840 900 gacgttgccatgaatgtcgccgaacagctgaaaaacaccggcaaagtccaacgcqgacaa gccagcggcgcattgattgccaaaatccttcccggcagccccgcagaacgtgccygcctg atcaatccgggcaattccggccggctgttcaacttaaaaggacaggtcgtcggcatc gacgttgccatgaatgtcgccgaacagctgaaaaacaccggcaaagtccaacgcggacaa caggoggagatatogtoctcagcotcgacggoggagaaatacgttottccgggogacett cccgtcatggtcggcgccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaa ggcgaagaaatcacaatcaaagccaagctgggcaacgccgagcatactacatca gcaggcattacccttcagacacataccgacagcagcagacaacacctcgtcgtacgg 1261 gcaggcattaccettcagacacataccgacagcagcggcggacggcttgtcgtcgtggg 1321 gtttccgacgcggcagaacgcgcaggcttaaggcacggcgacgaaatcctagccgtcagg Neisseria meningitidis strain ATCC 13090 BASB013 nucleotide ВЪ 98GB-0008734 99WO-EP02765 233305 standard; DNA; 1500 (first entry) 1381 gcaagtccccgtcaa 1395 1380 gcaagtccccgtcaa 1394 Neisseria meningitidis W09955872-A1 23-APR-1998; 21-FEB-2000 20-APR-1999; 04 - NOV - 1999 1021 1081 901 1021 1081 1141 721 901 961 1261 RESULT Z33305 g Dp Q g qq g ρp δ pp g q g qq ò ò οy ò ò ò ð ò ò ò

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SMITHKLINE BEECHAM BIOLOGICALS WPI; 2000-052809/04 P-PSDB; Y52993 (SMIK) Ruelle

polypeptides from Neisseria meningitis used t bacterial infections prepare vaccines against and polynucleotides Novel 9

Claim 15; Page 73-74; 94pp; English

The present sequence encodes a BASB013 polypeptide isolated from
Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be
employed as research reagents and material for the discovery of
treatments and diagnostics for diseases, particularly human diseases.
They can be used for diagnosts of disease, staging of disease, or
determining response of an infectious organism to drugs. The
polynucleotides may be used as a source for hybridisation probes, and
for screening of genetic mutations, serotype, organism or strain
identification, identification of mutation in BASB013 sequences, and as
components of arrays which are useful for diagnostic and prognostic
purposes. The polypeptides can be used to produce antibodies. The
polypeptides can also be used in vaccine formulations, and to identify
agonists and antagonists. The polypeptides, antibodies, agonists and
antagonists (which are bacteristatic) are used for the treatment and
prevention of diseases such as upper respiratory tract infection,
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invariant and managonists. The polyperiant mand meningitis, and meningitis, and meningitis, and meningitis, and meningitis, and meningitis, and meningitis. the development and screening of antibacterial drugs. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

Sequence 1500 BP; 370 A; 468 C; 393 G; 269 T; 0 other;

ij 240 240 180 480 tgcgaaaaaggcaggcagctttttcggtgcggacaaaaaagaagcatccttcgtagaacgc 120 Gaps 9 9 gtgttcaaaaaataccaatacctcgctttggcagcactgtgtgccgcctcgctggcaggc gtgttcaaaaaataccaatacttcgctttggcggcactgtgccgccttgctggcaggc atcgaacacacaaagacgacggcagtgtcagtatgctgctgcccgactttgcccaactg gttcaaagcgaaggcccggcagtcgtcaatattcaggcagccccgccccgcgcaccaa aacggcagcggcaatgccgaaccgattccgacccgcttgccgacagcgacccgttctac aacggcagcggcaatgccgaaaccgattccgacccgcttgccgacagcgacccgttctac gaatttttcaaacgcctcgtcccgaacatgcccgaaatcccccaagaagaagcagatgac acceacgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatat DB 21; Length 1500; ÷ 78; Indels Score 1258.2; Pred. No. 0; 0; Mismatches ô 90.2%; Query Match 90.2 Best Local Similarity 94.3 Matches 1316; Conservative 61 241 61 121 181 181 121 241 301 301 361 361 421 ð 9 ò Оb ò Q ö a ò q ò g ð 원 ò

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The NGSP polypeptide of N. gonorrhoeae has conserved Arg-Gly-Asp and Arg-Gly-Asn motifs near the C-terminus which function as adherence domains for extracellular matrix proteins. Using the NGSP polypeptide as a vaccine produces antibodies which inhibit binding of N. Gonorrhoeae to the host's cellular matrix reducing attachment and/or subsequent invasion. The NGSP polypeptide and its peptide fragments can be used to immunise an animal and produce an immune response. They can also be used as ligands to detect antibodies elicited in response to Neisseria infections and also as antigens or immunogens for inducting Neisseria-specific antibodies which are useful in immunoassays to detect Neisseria in biological specimens. Nucleotides encoding NGSP or its fragments can be used as probes to identify Neisseria in biological specimens by hybridization or polymerase chair reaction amplification. The NGSP polypeptide can also be used in screening assays to identify agents and compounds which useful as diagnostic, prophylactic or therapeutic agents against Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n-cytosolic NGSP polypeptide and polynucleotide sequence from isseria useful for diagnosis, prevention or treatment of Neisseria
                                                                  NGSP; polypeptide; peptide; vaccine; immune response; antibody; cellular matrix; adherence domain; ligand; detection; diagnosis; screening; probe; primer; prophylaxis; therapy; ss.
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P-PSDB; Y83151
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Similarity

Best Local Sim Matches 1242;

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214 61 274 121

Match

Query

840

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us-09-388-090-3.rng

573 420 633 480 753 900 813 099 873

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                        gaaatcccccaagaagaagcagatgacggcggattgaacttcggttcgggcttcatcatc
                                                              acaccetteatecaaacegacgttgccateaatecgggcaattecggeggeeggtgtte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
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                                                                                                                                 cytotoxic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednences
                                                                                                                               NMASP; non-cytosolic; antibacterial; antiinflammatory; cytotox
anti-NMASP antibody; vaccine; diagnosis; therapy; prophylaxis;
Neisserial infection; meningitidis; septicaemia; ds.
                                                                                                                                                                                                                                                  /product= "Neisseria meningitidis protein"
/transl_except= (pos:499..501, aa: Xaa)
/note= "Xaa is unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The protein sequence represented in SEQ ID NO:2 of specification is erroneous"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis NMASP polypeptide, nucleotide antibodies, useful in vaccines against infection
                                                                                                     encoding DNA
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Pred. No. 0;
0; Mismatches
                                                                                                      Neisseria meningitidis NMASP protein-1
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 41; Page 63; 75pp; English.
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ilarity 97.2%;
Conservative (
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                          Z51533 standard; DNA; 1347
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/*tag= a
                                                                            (first entry)
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                                                                                                                                                                                    Neisseria meningitidis
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Matches 1207; Conserv
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                                                                             03-JUL-2000
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                                                                                                                               NMASP; non-
anti-NMASP
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X98241 standard; DNA; 1436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a conserved BASB013-C polypeptide isolated from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be employed as research reagents and material for the discovery of treatments and diagnostics for diseases, particularly human diseases. They can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, antibodies, and to prevention of diseases such as upper respiratory tract infection, the progness of the diseases such as bacteriamia and meningitis, and for the body.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the development and screening of antibacterial drugs. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of
                                                                                                                                             Nelsseria meningitidis; BASB013; diagnosis; infection; vaccine; antibiotic; upper respiratory tract infection; bacteraemia; meningitis; invasive bacterial disease; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides and polypeptides from Neisseria meningitis used to prepare vaccines against bacterial infections
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                                                                                                                Neisseria meningitidis BASB013-C nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                  BP.
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                 233308 standard; DNA; 1110
                                                                               (first entry)
                                                                                                                                                                                                                 Neisseria meningitidis.
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962 ccagcggcgcattgattgccaaaatccttcccggcagcccgcagaacgtgccgqcctgc 1021
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                                122 tegaacaccaaaagaegaegaegeagegteagtatgetgetgeeegaetttgeeeaaet,,
                                                                           242 acggcagcgacatgccgaaaccgattccgacccgcttgccgacagcgacccgttctacg
                                                                                                                                                                                            242 acggcagcggcaatgccgaaaacgattccgacccgattgccgacaacgacccgttctacg
                                                                                                                                                                                                                                   302 aatttttcaaacgcctcgtcccgaacatgcccgaaatcccccaagaagaagcagatgacg
                                                                                                                                                                                                                                                                                                                 goggattgaacttoggttogggcttoatoatoagoaaaaaoggotaoatootgacoaata
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tcgaacacacaaagacgacggcagtgtcagtatgctgctgcccgactttgcccaact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522
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                                                                                                                                                                                                                                                                                                                  Mahajan-Miklos
                                                                                            Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection; ss
                                                                                                                                                                                                                                                                                                                                                                                             Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1436 BP; 267 A; 461 C; 471 G; 237 T; 0 other;
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                                                                                                                                                                                                                                                                                                                     Goodman HM,
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                                                                  Nucleotide sequence of the PA14 degP gene
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 27; 228pp; English
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66.0%;
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Fan M, Tsongalis
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                                                                                                                                                                                                                                                              97US-0066517
                                         (first entry)
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nes 544; Conservative
                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357851/30
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                                         25-OCT-1999
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Neisseria meningitidis; BASB013; diagnosis; infection; vaccine;
antibiotic; upper respiratory tract infection; bacteraemia; meningitis;
invasive bacterial disease; antibacterial; ss.
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                                                                                                                                                                                                                                                                                                                gogocattaogoogggaaaagaagtoagootoggogtatggogoaaaggogaagaaatoa 1153
                                                                                                                                                                                                                                                                                                                                     1063 gcaacatgaagccgggcgacaagatcaacctggacgtgattcgcaacggccagcgcaagt 1122
                                                                                                                                                                                                                    853
                                                                                                                                                  943 tggtggcgcagctggtggaagacggtccggcggccaagggcggcctgcaggtgggcgatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides and polypeptides from Neisseria meningitis to prepare vaccines against bacterial infections \,\cdot\,
                                                                                                                                                                           attccggcggccgctgttcaacttaaaggacaggtcgtcggcatcaattcgcaaatat
                                              acagecgeageggatteatgggeateteetttgecatecegattgaegttgecatga
                                                                                           atgtcgccgaacagctgaaaaacaccggcaaagtccaacgcggacaactgggcgtgatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis variable BASB013-V nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                             1154 caatcaaagccaagctyggcaacgccgcgcgagcataccggcgca 1197 | | | | | | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                 1123 ccttgagcatggcggtaggcaaccttccggacgacgacgaggaa 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis
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                                                                                                                                                                                                 Invasive bacterial diseases such as bacteraemia and meningitis, and for the development and screening of antibacterial drugs. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of
                                                     determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists which are bacteristatic) are used for the treatment and prevention of diseases such as upper respiratory tract infection,
                                                                                                                                                                                                                                                                                                                                                                                                                    aaagaagtcagcctcggcgtatggcgcaaaggcgaagaaatcacaatcaaagccaagctg 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagcaatccggtacgttctcggtcgaatccgcaggcattacccttcagacacataccgac 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1291 agcagoggcaaacacctcgtcgtcgtacgggtttccgacgcggcagaacgcgcaggctta 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be employed as research reagents and material for the discovery or treatments and diagnostics for diseases, particularly human diseases. They can be used for diagnosis of disease, staging of disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 aaagaagtcagcctcggcgtatggcgcaaaggcgaagaaatcacaatcaaagtcaagctg
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                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 390;
                                                                                                                                                                                                                                                                                                                                                           18.7%; Score 260.2; DB 21; Length 96.8%; Pred. No. 2.8e-61; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in-dwelling devices or by other surgical techniques.
                                                                                                                                                                                                                                                                                                                   Sequence 390 BP; 106 A; 120 C; 102 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product- htrA serine protease
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199..1674
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Matches 276; Conservative
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Best Local
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The sequence is that encoding the serine protease htrA which was used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442 ggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatcggttcg 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 gatgiccaatccgatgicgccttcigaaaalcgacgcaacggaagagciacccgicgic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 aaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcggcgcgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 aagatggcggattctgatgcactgcgcgtgggtgattacaccgtagggattggtaacccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             679 cccaacgaaagctacacaccttcatccaaaccgacgttgccatcaatccgggcaattcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847 aatgecgaaaactacgaaaactteateeagacegatgeagegateaaeegtggtaaetee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           907 ggtggtgggttggttaacctgaacggcgaactgatcggtatcaacaccgcgatcclcgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 799 cgcagcggcggattcatgggcatctcctttgccatcccgattgacgttgccatgaatgtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1027 acctcgcagatggtggaatacggccaggtgaaacgcggtgagctgggtattatggggact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 gtcatcattgatgccgataaaggctatgtcgtcaccaacaaccacgttgttgalaacgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607 acggtcattaaagttcaactgagcgatggccgtaagttcgacgcgaagatggttgycaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1854;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human serum protease protein(s) - used diagnosing pre-disposition to Alzheimer's disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.6%; Score 176.4; DB 19; Length
52.0%; Pred. No. 2.4e-38;
tive 0; Mismatches 386; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1854 BP; 478 A; 470 C; 489 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                 Karran EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clinkenbeard HE, Creasy CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 27-28; 65pp; English
                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
97EP-0306501
                                                        96US-0032875
                                                                                   96US-0025436
96US-0027873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the isolation of PSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 421; Conservative
                                                                                                                                                                                                                                                                                            Southan CD;
                                                                                                                                                                                                                                                                                                                                            WPI; 1998-161101/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W56771
26-AUG-1997;
                                                     13-DEC-1996;
06-SEP-1996;
                                                                                                              25-0CT-1996;
                                                                                                                                                                                                                                                              Browne MJ,
                                                                                                                                                                                                                                                                                            Livi GP,
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Search completed: March 22, 2001, 10:17:11 Job time: 25016 sec

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, KITK
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                       1 gtgttcaaaaaataccaata.......tcagggcaagtccccgtcaa 1395
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-245-294-7
US-08-474-499-7
US-08-307-279A-7
PCT-US95-06211-7
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US-09-106-467-1
US-08-485-569-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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US-08-483-859-1
US-08-472-173-1
US-08-487-167-1
US-08-296-149-1
US-08-296-149-1
US-08-801-499-1
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US-09-074-660-1
US-09-074-659-1
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                                                                                                                                                                                                                                                                                                                                                                                                                               280836 seqs, 80580151 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   using sw model
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seq length: 200000000
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Sequence 5, Appli
Sequence 3, Appli
Sequence 26, Appli
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US-08-923-454A-24
US-08-923-454A-30
US-08-923-454A-5
US-08-923-454A-3
US-08-923-454A-28
US-08-923-454A-26
US-08-440-856A-2
                                                                                                                                                                                                                              US-08-209-747-1
US-08-458-298-1
US-08-211-718-8
US-08-963-168C-1
US-08-963-168C-2
US-08-963-168C-2
US-08-461-775-9
US-08-461-775-9
US-09-031-606-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Southan, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-923-454A-13
; Sequence 13, Application US/08923454A
; Patent No. 6004794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
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944 GCGCTGCGCGTGGGGGATTATACCGTCGCTATTGGTAACCCGTTTGGTCTGGGCGAAACG 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 ctcaacgacaagcgcgaatataccgccaaactcatcggttcggatgtccaatccgatgtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1980;
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,741
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.6%; Score 175.6; DB 1
52.6%; Pred. No. 2.6e-39;
tive 0; Mismatches 364
                                                                                                              RELINGTON, 1100 NORTH GLEBE ROAD ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-MAR-1990
APPLICATION NUMBER: PCT/GB91/00484
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 00/952,737
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 07/952,737
FILING DATE: 30-NO-1992
APPLICATION NUMBER: GB 9007194.5
FILING DATE: 30-MAR-1990
                                                                                             ADDRESSEE: NIXON and VANDERHYE PC
                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                      TITLE OF INVENTION: LIVE VACCINES NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 20797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1980 base pairs
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
CHATFIELD S.N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Matches 407; Conserv
                                                                                                                                                            STATE: VIRGINIA
                                                                                                                                                                                                           22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-350-741-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
    APPLICANT:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1027 ACCTCGCAGATGGTGGAATACGCCCAGGTGAAACGCGGTGAGCTGGGTATTATGGGGACT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1087 GAGCTGAACTCCGAACTGGGGAAAGCGATGAAAGTTGACGCCCAGCGGGGGGTGCTTTCGTA 1146
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                                                                                                                                                            382 ggcttcatcatcagcaaaaacggctacatcctgaccaatacccacgtcgttgccggtatg 441
                                                                                                                                                                                                                                                                                    607 ACGGTCATTAAAGTTCAACTGACGATGGCCGTAAGTTCGACGCGAAGATGGTTGGCAAA 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727 AAGATGGCGGATTCTGATGCACTGCGCGTGGTGATTACACCGTAGGGATTGGTAACCCG 786
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                                                                                                                     Gaps
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                                                                                                                                                                                                      547 GTCATCATTGATGCCGATAAAGGCTATGTCGTCACCACAACAACCACGTTGTTGATAACGCG
                                                                                                                                                                                                                                                       442 ggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatcggttcg
                                                                                                                                                                                                                                                                                                                                                                                                667 GATCCGCCCTCTGATATCGCCCTGATCCAAATCCAGAACCCGAAAAACCTGACCGCAATT
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                                                                  Length 1854;
                                                                                                                Indels
                                                                  12.6%; Score 176.4; DB 3; 52.0%; Pred. No. 1.5e-39; ive 0; Mismatches 386;
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Patent No. 5804194
GENERAL INFORMATION:
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APPLICANT: CHARLES I.G.,
APPLICANT: HORMAECHE C.E.
APPLICANT: JOHNSON K.S.,
                                                               Query Match 12.6
Best Local Similarity 52.0
Matches 421; Conservative
US-08-923-454A-13
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1244 TACGGCCAGGTGAAACGCGGCGAACTGGGGATCATGGGGACTGAGCTGAATTCCGAATTG 1303
                                                                                                                                                                                                                                                      1304 GCGAAAGCGATGAAAGTCGACGCCCAGCGAGGCGCGTTCGTCAGCCAGGTGATGCCGAAT 1363
                                                                                                                                                                                                                                                                                                                                                          936
                                                                                                                                                                                                                                                                                                       ttaaaaaggacaggtcgtcggcatcaattcgcaaatatacagccgcagcggcggattcatg
                                                                                                                  ggcatctcctttgccatcccgattgacgttgccatgaatgtcgccgaacagctgaaaaac
                                                                                                                                                                       877 accggcaaagtccaacgcggacaactgggcgtgattattcaggaagtatcctacggtttg
                                                                                                                                                                                                                              997 agccccgcagaacgtgccggcctgcaggcgggcgacatcgtcctcagcctcgacggcgga
                                                                                                                                                                                                                                                                                                                                            gaaatacgttcttccggcgaccttcccgtcatggtcggcgccattacgccgggaaaagaa
                                                                                                                                                                                                                                                                                                                                                                                                   1117 gtcagcctcggcgtatggcgcaaaggcgaagaaatcacaatcaaagccaagctg 1170
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHATFIELD, Stewen N.
TITLE OF INVENTION: LIVE VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON and VANDERHYE PC
STREET: 81 FLY FLOOR, 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/463,875A
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/340,741
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US 07/952,737
30-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB 9007194.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER. IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08463875A Patent No. 2980907 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: DOUGAN, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHARLES, Ian G.
APPLICANT: HORMAECHE, CArlos E.
APPLICANT: JOHNSON, Kevin S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-MAR-1990
APPLICATION NUMBER: PCT/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: WILSON, MARY J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 30-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 30-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 8th FLOC
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-463-875A-1
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                                                                                                                                                                                                                                                                                                                                    Score 175.6; DB 2
Pred. No. 2.6e-39;
0; Mismatches 364
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                    Query Match 12.6%;
Best Local Similarity 52.6%;
Matches 407; Conservative
                  TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1980 base pairs
                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                        CDS
395..1822
                                                                                                                                                                               linear
                                                                                                                                                                                                                                   NAME/KEY:
COCATION:
US-08-463-875A-1
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Regnery, Russell L.
VENTION: METHODS AND COMPOSITIONS FOR METHODS AND ROCHALIMAEA HENSELAE VENTION: AND ROCHALIMAEA QUINTANA INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,499
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEEDLE & ROSENBERG, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.612
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,294
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08474499;
Patent No. 569376;
GENERAL INFORMATION:
APPLICANT: Anderson, Burt E.
APPLICANT: Requery, Russell L.
TITLE OF INVENTION: METHODS AND CGTILLE OF INVENTION: DIAGNOSING ROGITLE OF INVENTION: AND ROCHALIMAE NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgia
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STATE: Georgia
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                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: DIAGNOSING TITLE OF INVENTION: DIAGNOSING TITLE OF INVENTION: ROCHALIMAEA HENSELAE AND ROCHALIMAEA QUINTANA TITLE OF INVENTION: INFECTION NUMBER OF SEQUENCES: 10 CORRESSONDMENCE ADDRESS: ADDRESSE: NEEDLE & ROSENBERG, P.C. STREET: 127 PEACHLINE SIRGEL, SUITE 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacggaagagcta
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                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,294
                                                                              Regnery, Russell L.
VENTION: METHODS AND COMPOSITIONS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1%; Score 154.2; DB 1;
50.4%; Pred. No. 2.1e-33;
tive 0; Mismatches 393;
                                                                                                                                                                                                              3: NEEDLE & ROSENBERG, P.C.
127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SPICALL, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.612
TELECOMMUNICATION INFORMATION:
TELEFAN: 404/688-980
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 7, Application US/08245294
Patent No. 5644047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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EDNESS: double
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                                    GENERAL INFORMATION:
APPLICANT: Anderson,
APPLICANT: Regnery, F
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                                                                                                                                                                                                                                                                            Georgia
                                                                                                                                                                                                                                                    CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                          COUNTRY: U
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LOCATION:
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Best Local Si
Matches 403;
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673 agcotgoccaacgaaagctacacaccttcatccaaaccgacgttgccatcaatccgggc 732
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                                                                                         816 GATATCGGTACCGGTGTTTATGATGATTTTTATTCAGATTGATGCTGCAGTTAATTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            913 attcaggaagtatcctacggtttggcacagtcgttcggtctggataaagccagcggcgc
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APPLICANT: Regnery, Russell L
TITLE OF INVENTION: Nucleic Acids of Rochalimaea Henselae
TITLE OF INVENTION: and Methods and Compositions for Diagnosing Rochalimaea
TITLE OF INVENTION: Henselae and Rochalimaea Quintana Infection
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576 TOTGATGGCACAAGTTACGCTGTTGTTCTTGATGACGGTACAGAACTGAATGCAAAACTC 635
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                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       ADDRESSEE: NEEDLE & ROSENBERG, P.C. STREET: 127 Peachtree Street, N.E., Suite 1200 CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 154.2; DB 1;
Pred. No. 2.1e-33;
); Mismatches 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/307,279A FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 Sequence 7, Application US/08307279A Patent No. 5736347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-9880
INFORMATION FOR EG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1791 base pairs
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Similarity 50.4%;
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                                                                                                                   APPLICANT: Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                      GENERAL INFORMATION:
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US-08-307-279A-7
                                                 US-08-307-279A-7
                                                                                                                                                                                                                                                                                                               COUNTRY:
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Pred. No. 2.1e-33;
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                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                             11.18;
50.48;
                                                 LENGTH: 1791 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-474-499-7
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                                                                      aattocggcggccgctgttcaacttaaaaggacaggtcgtcggcatcaattcgcaata
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                                                                                                                                                                   TITICICCTICTGGGGGCAACGTTGGGATTGCTTTCGCTATTCCGGCAGCAACACGCAAC
                                 816 GATATCGGTACCGGTGTTTATGATGATTTATTCAGATTGATGCTGCAGTTAATCGAGGA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NEEDLE & ROSENBERG, P.C. STREET: 127 Peachtree Street, Suite 1200 CITY: Atlanta STATE: Georgia
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REFERENCE/DOCKET NUMBER: 1414.6121
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/245,294
FILING DATE: 18 MAY 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 7, Application PC/TUS95062111 ; GENERAL INFORMATION:
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NAME: Spratt, Gwendolyn D.
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TELEFAX: 404/688-9880
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TITLE OF INVENTION: ROCH
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 30303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           673 agcotgoccaacgaaagotacacaccottcatccaaaccgacgttgccatcaatccgggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  733 aattooggoogooogotgttoaacttaaaaggacaggtogtogoatcaattogcaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       936 TTTTCTCCTTCTTGGGGCAACGTTGGGATTGCTTTCGCTATTCCGGCAGCAACAGGGGAAC
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                                                                                                                                                                                                                                                                                                               Length 1791;
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                                                                                                                                                                                                                                                                                                        Score 154.2; DB 4;
Pred. No. 2.1e-33;
0; Mismatches 393;
                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1153 acaatcaaagccaagctgg 1171
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                                                                                                                                                                                                                                                                                                               11.1%;
50.4%;
                                                                                                                                                                                                                                                                                                                                                                      403; Conservative
                             double
                                                                                                                                                    CDS
141..1649
nucleic acid
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 403; Conserva
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1648 GGCGAACTCAATGCTGATTTAGCCAAAGCCTTTAATGTAAGCGCGCAACAAGGCGCATTT 1707
                                                                                                                                                                                                                                                                                                                                                1708 GTAAGTGAAGTTTTACCGAAATCTGCTGCTGAAAAAGCGGGACTTAAAGCGGGCGATATT 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1036 gtcctcagcctcgacggcggagaaatacgttcttccggcgaccttcccgtcatggtcggc 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1468 TCGGGTGGAGCGTTAGTAAACTTAAATGGCGAACTTATTGGAATTAATACCGCAATTATT 1527
                                                                                                                                                                                                                                                  916 caggaagtatcctacggtttggcacagtcgttcggtctggataaagccagcggcgattg 975
                                                        796 agccgcagcggcggattcatgggcatctcctttgccatcccgattgacgttgccatgaat 855
                                                                                                                                                      856 gtcgccgaacagctgaaaaaacaccggcaaagtccaacgcggacaactggggcgtgattatt 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1096 gccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggcgaa 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Analog of Haemophilus Hin
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR PLICATION DATA:
APPLICATION NUMBER: US 08/278,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08483859
Patent No. 5656436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, RAYMOND P.
APPLICANT: KLEIN, MICHEL H.
TITLE OF INVENTION: Reduced Pr
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-JUL-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Suite 701
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1168 GATAAAATTACCGTGCAATTACAAGATGGGCGTGAATTTAAAGCAAAATTAGTGGGTAAA 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1228 GATGAACTATCAGATATTGCATTAGTACAGCTTGAAAAACCAAGTAATTTAACAGAAATC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 ttcggctttgacaacagcgtgaccgccggcatcgtgtccgccaaagg-----cagaagc 675
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                                                                                                                                                                                                 Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
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APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 139.4; DB 1;
Pred. No. 3.1e-29;
0; Mismatches 381;
                                                                                                                                                                                                                                                                                             ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CTTY: Troonto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 1, Application US/08278091
Patent No. 5506139
Patent No. 5506139
PAPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: Applicant Reduced Proteet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPANCE: (416) 595-1155
TELEPANCE: (416) 595-1163
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS: 1:
LENGTH: 2894 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.0%;
Best Local Similarity 49.8%;
Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-278-091-1
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 49.8°
Matches 384; Conservative
                                                                                                                           ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: PatentI
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-472-173-1
                                                                                                                Canada
                                                                                CITY: Toronto
STATE: Ontario
                                                                                                                                                                                COMPUTER:
                                                                                                                COUNTRY:
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                                                                                                                                                              GATAAAATTACCGTGCAATTACAAGATGGGCGTGAATTTAAAGCAAAATTAGTGGGTAAA 1227
                                                                                                                                                                                                                                                                                                      GATGAACTATCAGATATTGCATTAGTACAGCTTGAAAAACCAAGTAATTTAACAGAAATC 1287
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                                                                                                                Gaps
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                                                                                Length 2894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1096 gccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggcgaa 1146
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                                                                               DB 1;
                                                                                                             0; Mismatches 381;
                                                                                               Pred. No. 3.1e-29
                                                                             10.0%; Score 139.4; 49.8%; Pred. No. 3.1e
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Patent No. 5665353
GENERAL INFORMATION:
                                                                                                             384; Conservative
; STRANDEDNESS: Sir; TOPOLOGY: linear US-08-483-859-1
                                                                                               Similarity
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                                                                               Query Match
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1108 GTCATTATTAATGCAAGCAAAGGCTATGTTTTAACCAATAATCATGTTATTGATGATGATT 1167
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PatentIn Release #1.0, Version #1.25
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0; Mismatches 381;
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ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
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APPLICATION NUMBER: US/08/472,173
FILLING DATE: 07-JUN-1995
FILLING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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IBM PC compatible
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1588 TTAGTGCAACAATTTTAGAATTTGGTCAAGTGCGTCGCGGATTGCTTGGTATTAAAGGT 1647
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                                                                       gtcgccgaacagctgaaaaacaccggcaaagtccaacgcggacaactgggcgtgattatt 915
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Rele
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: RUEIN, Michel H.
APPLICANT: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
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CIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-508 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/487,167
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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FILING DATE: 26-AUG-1994
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FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08487167
Patent No. 5869302
GENERAL INFORMATION:
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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US-08-487-167-1
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APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: XLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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    Length 2894;
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                                            Indels
Score 139.4; DB 2;
Pred. No. 3.1e-29;
0; Mismatches 381;
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Patent No. 5935573
GENERAL INFORMATION:
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
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1648 GGCGAACTCAATGCTGATTTAGCCAAAGCCTTTAATGTAAGCGCGCAACAAGGCGCGTTTT 1707
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                                                                      916 caggaagtatcctacggtttggcacagtcgttcggtctggataaagccagcggcqcattg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
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                                                                                                                                                                                                                                                                                                                                                                                        1828 ACCACTGGTGCAGGCAAAGAGATTAGCTTGACTTACCTTACGTGATGGCAAA 1878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 139.4; DB 2;
49.8%; Pred. No. 3.1e-29;
tive 0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--wentrer: IBM PC compatible
--wentrer: YeareM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOGSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Reduced Prot
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08296149 Patent No. 5939297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2894 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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PatentIn Release #1.0, Version #1.25
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Pred. No. 3.1e-29
Suite 701, 330 University Avenue
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                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INPORMATION:
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1155
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                          COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
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49.8%;
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Ontario
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Best Local 3
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1108 GTCATTATTAATGCAAGCAAAGGCTATGTTTTAACCAATAATCATGTTATTGATGAAGCT 1167
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Pred. No. 3.1e-29;
0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                   1038-671 MIS: jb
                                                                                                                                                                     FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/296,149
PRIOR APPLICATION NUMBER: US 08/770
                                                                                                                APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-JUN-1995
                      US/08/801,499
                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 49.8%;
Matches 384; Conservative
                                                                                                                                                                                                                                                                                   FILING DATE: 21-JUL-1994 ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                       1528 TCTCCAAGCGGTGGCAATGCAGGAATTGCCTTTGCGATTCCAAGTAATCAAGCAAT 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       976 attgccaaaatccttcccggcagcccgcagaacgtgccggcctgcaggcggcgacatc 1035
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ggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatcggttcg 501
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6th Floor, 330 University Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
PPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
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CITY: Toronto
STATE: Ontario
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                                   1708 GTAAGTGAAGTTTTACCGAAATCTGCTGCTGAAAAAGCAGGACTTAAAGCGGGGGGATATT 1767
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APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: YONG, Pele
APPLICANT: GOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: RIEIN, MICHEL H.
APPLICANT: RIEIN, MICHEL H.
APPLICANT: RIEIN, MICHEL H.
APPLICANT: RIEIN, MICHEL H.
APPLICANTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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Pred. No. 3.1e-29;
0; Mismatches 381;
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6th Floor, 330 University Avenue
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
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Best Local Similarity 49.8%;
Matches 384; Conservative
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MEDIUM TYPE: Floppy
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COUNTRY:
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Sequence:
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                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                       Run on:
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gb_est70:*

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AM742283 UP55810.7

AM159029 V283808.r

AM654015 10226 MA
W17262 22b17808.r1

AW664044 99913 MAR

F07134 HSCLM6081 n

AV611726 AV614726

AV59976 AV599976

AV599976 AV599976

AV51726 AV61427

AV61726 AV61427

AV667427 AV667427

AV667427 AV667427

AV667427 AV667427

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AV67427 AV667427

AV667427 AV693667

AV66762 AV69367

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AV66762 AV69667

AM462230 BP230008B

AV66730 BP230008B

AV66737 AV60003
                                                                                                                      AA479844 zu43h07.r
AW491392 U1-M-BH3-
AA110074 mo51b12.r
                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA479844 490 bp mRNA EST 09-NOV-199 zu43h07.rl Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:740797 5' similar to SW:HTRA_SALTY P26982 PROTEASE DO PRECURSOR; mRNA sequence.
AA479844 GI:2205730 EST.
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AW446594 6
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BE236269
BE236299
AV614725
AW462478
AA349615
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140 F08513
141 H42958
138 AA013197
134 BE02667
134 BE026655
134 AA54554
14 H16043
13 AA913980
15 AA913980
15 AA913980
18 BE754831
19 AA913980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA254878
6 BE843509
4 BE055938
AW632119
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9b_gss26:*
9b_gss27:*
9b_gss28:*
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Match
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AA479844
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gb_est58:*

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em_gss2:*
em_gss3:*
em_gss4:*
gb_gss5:*
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91674 N

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Mammalist Eutheria; Filmates, Catalling, Dominists, Comparison of the Mammalist Eutheria; Filmates, Catalling, Dominists of the 490)

Krizman, D., Kucaba, T., Lacy, M., Lehnon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Lehnon, G., Marra, M., Martin, J., Moore, B., Schellenberg, R. and Wilson, R. White, Y., Wylie, T., Waterston, R. and Wilson, R. Gontact: Wilson RF Project

Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wateson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2408 Std Error: 0.00

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 417.
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                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 CAGTCACCACCGGGATCGTGAGCACCACCAGGGGGGCGACAAAGAGCTGGGGCTCCGCA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaaacggctacatcctgaccaatacccacgtcgttgccggtatgggcagtatcaaagtcc 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AAGATGGACTGATCGTGACAAATGCCCACGTGGTGACCAACAAGACGGGTCAAAGTTG 70
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pred. No. 6.7e-18;
0; Mismatches 164; Indels 12
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                              Chordata;
Primates;
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Mammalia; Eutheria;
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                Homo sapiens
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SOURCE
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JOURNAL
COMMENT
                                                                    REFERENCE
                                                                                    AUTHORS
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/db_xref="taxon:1000"
/db_xref="taxon:1000"
/clone="UI"-WIH:BMAP_W_S4"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/lab_host="DH108 (Life Technologies)" with a modified
/note="betto" pr773D-pac (Pharmacia) with a modified
/note="vector: pr773D-pac (Pharmacia) with a modified
/note="betto" pr773D-pac (Pharmacia) with a modified
/note="libraries from to regions of the mouse brain
normalized libraries from to regions of the mouse brain
normalized libraries from to regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hipoccampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
wer generated in this process: NIH_BMAP_W_S3.1,
NIH_BMAP_W_S3.3, NIH_BMAP_W_S3.2, NIH_BMAP_W_S3.1,
NIH_BMAP_W_S3.3, NIH_BMAP_W_S3.3, NIH_BMAP_W_S3.2,
And NIH_BMAP_W_S3.3, NIH_BMAP_W_S3.3, NIH_BMAP_W_S3.2,
and constructed as follows: PCRamplified
was used as a driver in a hybridization with a pool of
the NIH_BMAP_W_S3.3, NIH_BMAP_W_S3.3, and NIH_BMAP_W_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mEST@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligo-drollectide that was used to prime the synthesis of first cligoridectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases; I to 479)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                        UI-W-BH3-atr-e-02-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-W-BH3-atr-e-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                            24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chin, H
National Institute of Mental Health
(5001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
cgctgttcaacttaaaaggacaggtcgtcggcatcaa 782
                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                               AW491392.1 GI:7061638
                                                                                                                                                                                                                                   479 bp
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AW742283 660 bp mRNA EST 07-5EP-2000 up55a10.yl Soares_mouse_NMIE Mus musculus cDNA clone IMAGE:2779962 5' similar to TR:092743 Q92743 NOVEL SERINE PROTEASE. ; mRNA
                                                                                                                                                                                                                                                                                                                                         /noter"Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: 0190 dT. 10.5dpc embryos. pCMV-SPORT2 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butolcostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (Info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Mus musculus"
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/clone="lib="Life Tech mouse embryo 10 5dpc 10665016"
/tssue_type="embryo"
/dev_stage="10.5dpc embryos"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 cgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatalaccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 attgaacttcggttcgggcttcatcatcagcaaaaacggctacatcctgaccaatacce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 TGCCATTGGAAGCCCCTTTTCTCTTCAAAACACAGTCACCACTGGGATCGTCAGCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 7.0%; Score 97.4; DB 2; Length 489; Local Similarity 53.8%; Pred. No. 5.5e-17; les 231; Conservative 0; Mismatches 186; Indels 1
                                             Janus.
MGI:337879
Seg primer: -28M13 rev1 from Amersham
High quality sequence stop: 446.
Location/Qualifiers
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converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NHLBMAP_MS4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 7AG_LIB-NHLBMAP_M_S4
TAG_TISSUE-corpus-striatum
TAG_TISSUE-corpus-striatum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 489)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 gtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcggc 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 AATTATGGAATTCCGGAGGCCCGTTAGTAAACCTGGATGGCGAGGTGATTGGGATTAA 57
                                                                                                                                                                                                                                                                                                                                                             ggttcgggcttcatcatcagcaaaaacggctacatcctgaccaatacccacgtcgttgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                               436 ggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatc
                                                                                                                                                                                                                                                                                                                                                                                                    475 GGGTCAGGATTCATCGTATCGGAGGATGGACTGATTGTGACAAATGCTCACGTGGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 gcgcccttcggctttgacaacagcgtgaccgccggcatcgtgtccgccaaaggcagaagc
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                     Score 98.6; DB 91; Length 479;
Pred. No. 2.5e-17;
0; Mismatches 179; Indels 12
                                                                                                                                                                                    143 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                   228; Conservative
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                             1. .660
/organism="Mus musculus"
/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="INAGE:2779962"
/clone="INAGE:2779962"
/clone="Inha"
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/lab_host="DH10B"
//dev_stage="newborn"
/lab_host="DH10B"
//dev_stage="newborn"
/lab_host="DH10B"
/dev_stage="newforn"
/lab_host="DH10B"
/dev_stage="newforn"
/lab_host="Conner are inner ear, 170 pooled; Vector: pT7T3D-Pac;
Site_1: Not I: Site_2: Eco RI: 1st strand cDNA was primed with a Not I: oligo(dT) primer [5'
Site_1: Not I: oligo(dT) primer [5'
Site_1: Not I: oligo(dT) primer [5'
Site_1: Not I: oligo(dT) primer [5'
Ind not I: oligo(dT) primer [5'
Ind Eco RI: sites of the modified pT7T3 vector: Library is normalized, and was constructed and donated by Bento Soares and M. Fatina Bonaldo (University of Iowa) and R. Hardisty, A. Varela-Carver, P. Mburu and S.D.M. Brown (MRC UN MAC) and Manmalian Genetics Unit,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 TGCCATTGGAAGCCCCTTTTCTCTTCAAAACACAGTCACCACTGGGATCGTCAGCACCAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         713
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                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacgga 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 attgaacttcggttcgggcttcatcatcagcaaaaacggctacatcctgaccaataccca 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 CGTGGTCACCAACAAAAACCGGGTCAAGGTTGAGCTGAAGAATGGAGCTACCTATGAAGC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 aqaqctacccgtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 aggcagaagc-----ctgcccaacgaaagctacacccttcatccaaaccga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 94; Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 97.4; DB 94
53.8%; Pred. No. 5.9e-17;
Live 0; Mismatches 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 t
                                                                                                                                                                                High quality sequence stop: 431.
Location/Qualifiers
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154 c
                                        Tumor Gene Index
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     AUTHORS
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/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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                                                                                                                                                                                      Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 456)
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
  AII59029 456 bp mRNA EST 02-OCT-1998 vz83a08.rl Soares_mammary_gland_NDMMG Mus musculus CDNA clone IMAGE:1333046 5' similar to TR:Q92743 Q92743 NOVEL SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 ggttcgggcttcatcatcagcaaaaoggctacatcctgaccaatacccacgtcgttgcc 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 ggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatc 495
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02-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 241.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/db.mdE=:1333046"
/clone="iMAGE:1333046"
/sex="male"
/tissue_type="mammary_gland"
/tasue_type="mammary gland"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 95.4; DB 16;
53.9%; Pred. No. 2e-16;
iive 0; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M.Mouse EST Project
Washi-HHM Mouse EST Project
Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .456 //Organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 g
                                                                                                                     AI159029.1 GI:3692211
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AI159029
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source
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Cetartiodactyla; Ruminantia: Pecora; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; Lossas I to 521)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                 615
                                                                                                                                   675
                                                                                      250 AGCCCCTTTTCTCTTCAAAACACAGTCACCACTGGGATCGTCAGCACCACCAGCGAGGC 309
                                                                                                                                                                                                   ------ctgcccaacgaaagctacacacccttcatccaaaccgacgttgccatc 723
                                                                                                                                                                                                                                   616 gegecetteggetttgacaacagegtgacegecegeatcgtgtcegecaaaggeagaage
                               130 GATGTGGATGAAAAGGCGGACATTGCGCTTATCAAGATTGACCACCAGGGAAAGCTGCCA
                                                                 gtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 94.6; DB 93; Length 521;
Pred. No. 3.5e-16;
0; Mismatches 194; Indels 12
                                                                                                                                                                                                                                                                                                                                                                             AW654015 521 bp mRNA EST 1
103326 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW654015
AW654015.1 GI:7419841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4890
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 103 row: D column: 5
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Best Local Similarity 53.1%; Matches 233; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Smith TPL
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ORIGIN
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AUTHORS
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                                                                 256
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VERSION
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SOURCE
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366 attgaacttcggttcgggcttcatcatcagcaaaaacggctacatcctgaccaatacca 425

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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.

1 (bases 1 to 474)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT773D (Pharmacla) with a
modified polylinker; Site_l: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortuum (info@lmage.linl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop: 446.
Location/Qualiflers
545
                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                  605
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IMAGE:302294 5' similar to SW:HTRA_SALTY P26982 PROTEASE DO
                                                                                                                                                                                     486 caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacgga
                                                                                                                                                                                                                    546 agagetaccegtegteaaaateggeaateceaaaaatttgaaaeeegggegaatgygtege
                                                                                                                                                                                                                                                                                                                                                                                                       606 tgccatcggcgcgccttcggctttgacaacagcgtgaccgccggcatcgtgtccgccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                         308 CGCCATTGGAAGCCCGTTTTCCCTTCAAAACACGGGTCACCACGGGGATCGTCAGCACCAC
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                                                                           426 cgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatalaccgc
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Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:1247226"
/db_xref="taxon:9606"
/clone="IMAGE:302294"
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W17262.1 GI:1291697
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1 (bases 1 to 504)
Smith, T. P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, M.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,
W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
Unpublished (2000)
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 gtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcggc 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 ggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatc 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggttcgga.tgtccaatccgatgtcgcccttctgaaaatcgacgcaacggaagaggtaccc 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GGGTCTGGGTTTATTGTGTCGGAAGATGGACTGATCGTGACAAATGCCCACGTGGTGACC 64
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AW660844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            616 gegeeetteggetttgacaacagegtgacegeeggeategtgteegea
              /organism="Homo sapiens"
/db_xref="Gals-41500"
/db_xref="taxon:9606"
/clone="IMAGE:38967"
/clone="Lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92.2; DB 144;
Pred. No. 1.6e-15;
); Mismatches 123;
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ilarity 57.4%;
Conservative
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Matches 166; Conserv
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LOCUS
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1 (bases I to 485)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-warck EST Project
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                           ;
0
double stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHH19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 1476
High quality sequence stops: 391 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1476 Std Error: 0.00
Seq primer: M13RP1
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                                                                                                                                                                                                                                                                                                                                                                                                       41 GGGTCTGGGTTTATTGTGTCGGAAGATGGACTGATCGTGACAAATGCCCACGTGGTGACC 100
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yg75a09.rl Soares infant brain 1NIB Homo sapiens CDNA clone
IMAGE:38967 5' similar to SP:HTRA_SALTY P26982 PROTEASE DO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                              Score 92.2; DB 146; Length 474; Pred. No. 1.6e-15;
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                                                                                                                                                                                                                                                                                                                           0; Mismatches 123;
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Best Local Similarity 57.4%;
Matches 166; Conservative
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Email: genexpress@genethon.fr
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v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                           /note-"Vector: pCMV SPORT6; Site_1: Xba1; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

143 c 146 g 102 t
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HSClWG081 normalized infant brain cDNA Homo sapiens cDNA clone
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Genethon Centre de recherche sur le Genome Humain
L'rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
191: 33169472808
Fax: 33160778698
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95277534
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 91; DB 93; Length 5C llarity 56.5%; Pred. No. 3.6e-15; Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                                /clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"

    504
    /organism-"Bos taurus"

                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 101 row: N column: 22
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                  /db_xref="taxon:9913"
                                      PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                          Location/Qualifiers
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/issue_type."total brain."
//dev stage="3 months old"
//octe."Organ: brain: vector: lafmid BA; Site_1: HindIII:
//octe."Organ: brain: vector: lafmid BA; Site_1: HindIII:
//octe."Organ: brain: vector: dev_stage-3 months old;
//octe. MRNA was oligo-(dT) primed and directionally
//octe. Total mRNA was oligo-(dT) primed and directionally
//octor. Clone library from B. Soares, Psychiatry
//octe. Columbia University, USA. Normalization_method:
//octer. 100 g 66 t 1 others
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
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Seq primer: (-21)Ml3_universal.
Location/Qualifiers
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AV614726 Bos taurus adipocyte cell line Bos taurus cDNA clone
ElAD006406 5', mRNA sequence.
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/clone-1c-1wg08"
/clone-1lb-"normalized infant brain cDNA"
/sex-"Female"
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Pred. No. 8.2e-15;
0; Mismatches 125; Indels
                                                                                                                        /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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Sugimoto, Y., Hirotsune, S.,
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AV614726.1 GI:9750396
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Best Local Similarity 56.7%;
Matches 164; Conservative
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rel: +55-11-2704922
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1 (bases 1 to 559)
                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElAD006406"
/clone_lib="Bos taurus adipocyte cell line"
/cell_type="an adipocyte cell line"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A was deleted from a Not1 site"
139 c 149 g 108 t lothers
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                                                                                                                                                                                                                                                                                                                                                 366 attgaacttcggttcgggcttcatcatcagcaaaacggctacatcctgaccaataccca 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgccatcggcgcgccttcggctttgacaacagcgtgaccgccggcatcgtgtccgccaa 665
                                                                                                                                                                                                                                                                                                                                                                                                                   cgtcgttgccggtatggggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgc 485
                                                                                                                                                                                                                                                                                                                                                                                                                                             170 CGTGGTGACCAACAAGCATCGGGTCAAAGTCGAGCTTAAGAATGGTGCCACCTATGAGGC 229
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bovine cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shizakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 agagctacccgtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AAAGCIGCCIGIGCIACTGCTIGGCGGCTCCICGGAGCIGCGGGGGGGAGAGIICGIGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacgga
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714 cgttgccatcaatccgggcaattccggcggcccgctgttcaacttaaaaggacaggtcg
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W599976 Bos taurus cartilage fetus Bos taurus cDNA clone
E1CAO47C06 5', mRNA sequence.
AV599976
                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                         Length 529;
                                                                                                                                                                                                                                                                                      Score 89; DB 37; Length 52:
Pred. No. 1.4e-14;
0; Mismatches 185; Indels
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                      6.4%;
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1. .559
/organism="bos taurus"
/organism="bos taurus"
/db_xref="taxon:9913"
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/clone_lip="Bos taurus cartilage"
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/tissue_type="cartilage"
/dev_stage="fetus"
/dev_stage="fetus"
/lab.host="DH108"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
35 a 158 c 158 g 108 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 ACTGGCCAGTGGGTCTGGTTCATCGTGTCGAAGATGGACTGATTGTGACAAACGCCCA 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 AAAGCTGCCTGTGCTACTGCTTGGCCGCTCCTCGGAGCTGCGGCGGGAGAGTTCGTGGT 407
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QV-BT032-190299-136 BT032 Homo sapiens cDNA, mRNA sequence.
A1903651
                                                                                 Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87.8; DB 37;
Pred. No. 3.1e-14;
0; Mismatches 132;
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
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Best Local Similarity 55.9%;
Matches 167; Conservative
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Unpublished (1995)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: breast, Vector: puc18; Site_1: SmaI: Site_2: SmaI: A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
Fax: +55-11-2707001
Email: asImpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT032-136.html
&t3=190299&t4=1)
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1 (bases 1 to 518)
1 (bases 1 to 518)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 CCCACACGGTGTCGTCCAGGGGGGGGGGGTCCCTGGGCTCGGGCTTATCATTTGCCAG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 TGAAGGCTACGTGCTGACCAACAACCCGATGGTCGCGGACGACGACGAGATCATCGTCTG 211
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Best Local Similarity 55:9%; Pred. No. 7.6e-14;
Matches 185; Conservative 0; Mismatches 143;
                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone_lib="BT032"
/sex-"female"
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Contact: Wilson RW
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estéwatson.wustl.edu
Insert Size: 1522
High quality sequence stops: 453 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 ggtatgggcagtatcaaagtcctgctcaacgacaagcgaatataccgccaaactcatc 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AACAAGCACCGGGTCAAAGTTGAGCTGAAGAACGGTGCCACTTACGAAGCCAAAATCAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 ggttcggatgtccaatccgatgtcgccttctgaaaatcgacgcaacggaagagctaccc 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GTCCTGCTGCTTGGCCGCTCCTCAGAGCTGCGGCCGGGGAGANTTCGTGGTCGCCATCGGA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 gtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGTCTGGGTTTATTGTGTGGAAGATGGACTGATCGTGACAAATGCCCACGTGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 GATGTGGATGAGAAAGCAGACATCGCACTCATCAAANTTGACCACCAGGGCAAGCTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84.2; DB 144; Length 518;
Pred. No. 3.2e-13;
0; Mismatches 120; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:31324"
/clone_lib-"Soares infant brain 1NIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AGCCCGTTTTCCCTTCAAAACACAGTCACCACCGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 gegecetteggetttgacaacagegtgacegeegg
                                                                                                                                                                                                                                                                                                                                                                                                             /organism~"Homo sapiens"
/db_xref="GDB:403671"
/db_xref~"taxon:9606"
                                                                                                                                                                                                                                                                                                   Seg primer: M13RP1
High quality sequence stop: 453
Location/qualiflers
1..518
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Job time: 4478 sec
                                      Tunidation, Lucinitary Filiates, Catallinin, Domininger, Homon.

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The WashU-Marck EST Project
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was ligated to Hind III adaptors (Pharmacla), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 143 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Insert Length: 1530 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 teggitegggetteateateageaaaaeggetacateetgaceataceeggegteg 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 coggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactca 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 CCAACAAGCACCGGGTCAAAGTTGAGCTGAAGAACGGTGCCACTTACGAAGCCAAAATCA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 teggiteggaigtecaateegaigtegeeetteigaaaategaegeaaeggaagageiae 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 ccgtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 81.2; DB 146; Length
53.7%; Pred. No. 1.9e-12;
tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 288
/organism="Homo sapiens"
/db_xref="GDB:397142"
/db_xref="taxon:9666"
/clone="IMAGE:24795"
/clone_lib="Soares infant brain INIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gegegeeetteggetttgacaacagegtgacegeeggeategt 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 143.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 53.7
Matches 152; Conservative
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                                             REFERENCE
AUTHORS
                                                                                                                                                                  TITLE
JOURNAL
COMMENT
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Search completed: March 22, 2001, 03:35:13

Fri Mar 23 07:26:57 2001

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